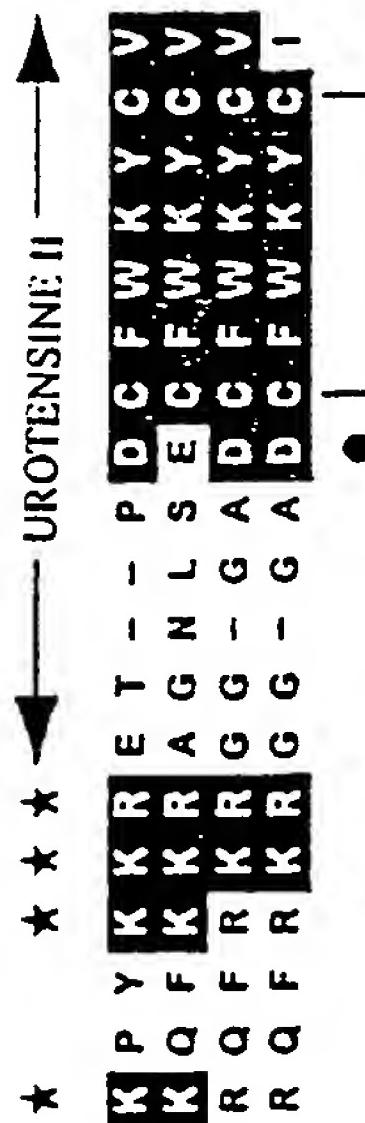


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Humain	-M-Y-K-L-A-S-C-C-L-L-F-I-G-F-L-N-P-L-L-S-L-P-L-L-D-S-R-E-I-S-F-Q-L-S-A-P-H-E-D-A-R-L-T-P-E-E-L-E-R	49
Grenouille	-M-S-K-L-F-F-C-C-L-I-L-A-G-S-F-C-S-F-R-S-L-P-I-I-V-P-S-K-G-B-L-R-L-S-E-S-A-L-D-F-G-D-L-K-S-W-D-D-E	49
Carpe $\alpha$	M-M-C-N-L-L-S-F-S-V-L-L-S-C-T-H-U-V-A-H-P-V-T-D-T-A-D-M-T-Y-S-G-P-D-S-V-E-E-A-G-C-V-S-E-A-G-G-V-N-S-G-P-D-S-V-E-E-A-G-G-V	49
Carpe $\gamma$	M-M-C-N-L-L-S-C-S-V-L-L-S-C-S-H-L-L-A-H-P-V-T-D-T-A-D-M-T-Y-S-G-P-D-S-V-E-E-A-G-G-V-N-S-G-P-D-S-V-E-E-A-G-G-V	49
		96
Humain	A-S-T-L-Q-I-L-P-E-M-L-G--A-E-R-G--D-I-L-R-K-A-D-S-S-T-N-I-F-N-P-R-G-N-L-R-K-F-Q-D-P	96
Grenouille	T-R-L-L-R-N-L-P-M-F-V-D-K-E-A-E-D-F-S-K-E-C-F-G-L-D-A-Y-N-M-D-K-E-E-L-F-D-K-H-P-R--	96
Carpe $\alpha$	A-V-S-D-L-N-O-L-L-Q-R-A-A-V-V-E-Y-S--P-L-L-S-R-E-N-I-K-V-P-G-Q-I-P-K-E-A-L-R-E-L-L-E-K-P-Y--	96
Carpe $\gamma$	S-V-S-D-L-N-E-H-L-Q-R-A-A-V-A-G-Y-S--P-L-F-S-Q-E-N-I-K-V-P-G-Q-I-P-K-E-A-L-R-E-L-L-E-K-P-Y--	96



Human	N-I-L-L-S-H-L-A-R-I-W-K-P-Y-K-K-R-E-T--P-D-C-F-W-K-Y-C-V	124
Grenouille	I-S-L-L-S-R-L-Q-F-K-K-R-A-G-N-L-S-E-C-F-W-K-Y-C-V	127
Carpe $\alpha$	R-L-I-P-P-S-G-L-W-G-S-R-R-Q-F-R-K-R-G-G-C-A-D-C-F-W-K-Y-C-V	126
Carpe $\gamma$	R-L-I-P-P-R-G-L-W-G-S-R-R-Q-F-R-K-R-G-G-C-A-D-C-F-W-K-Y-C-V	126

FIGURE 1

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CCAAGAAGGAAGCCGTCTATCTTGTGGCGATC

ATG TAT AAG CTG GCC TCC TGC TGT TTG CTT TTC ATA GGA TTC TTA  
 Met Tyr Lys Leu Ala Ser Cys Cys Leu Leu Phe Ile Gly Phe Leu

**PEPTIDE SIGNAL**

AAT CCT CTC TTA TCT CTT CCT CTC CTT GAC TCC AGG GAA ATA TCC  
 Asn Pro Leu Leu Ser Leu Pro Leu Leu Asp Ser Arg Glu Ile Ser

TTT CAA CTC TCA GCA CCT CAT GAA GAC GCG CGC TTA ACT CCG GAG  
 Phe Gln Leu Ser Ala Pro His Glu Asp Ala Arg Leu Thr Pro Glu

**PRO-SEGMENT**

GAG CTA GAA AGA GCT TCC CTT CTA CAG ATA CTG CCA GAG ATG CTG  
 Glu Leu Glu Arg Ala Ser Leu Leu Gln Ile Leu Pro Glu Met Leu

GGT GCA GAA AGA GGG GAT ATT CTC AGG AAA GCA GAC TCA AGT ACC  
 Gly Ala Glu Arg Gly Asp Ile Leu Arg Lys Ala Asp Ser Ser Thr

AAC ATT TTT AAC CCA AGA GGA AAT TTG AGA AAG TTT CAG GAT TTC  
 Asn Ile Phe Asn Pro Arg Gly Asn Leu Arg Lys Phe Gln Asp Phe

TCT GGA CAA GAT CCT AAC ATT TTA CTG AGT CAT CTT TTG GCC AGA  
 Ser Gly Gln Asp Pro Asn Ile Leu Leu Ser His Leu Leu Ala Arg

ATC TGG AAA CCA TAC AAG AAA CGT GAG ACT CCT GAT TGC TTC TGG  
 Ile Trp Lys Pro Tyr Lys Lys Arg Glu Thr Pro Asp Cys Phe Trp

**UROTENSINE II**

AAA TAC TGT GTC TGA  
 Lys Tyr Cys Val \*\*\*

AGTGAAATAAGCATCTGTTAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACA  
 ATGCTTGATTGAAAACAGTGTGGAGAAAAACTAGGCCAAACTACACCCTGTTATTGTTACCT  
 GGAAAATAATCCTCTAT

**FIGURE 2**

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9            18            27            36            45            54  
 5' CGG AGC AGA CAC CCA GCC AGA CTT CTT CCC GTC GTC ATG GAC AGG GTG CCC TTC  
 Met Asp Arg Val Pro Phe  
 ↓.....

63            72            81            90            99            108  
 TGC TGC CTG CTC TTC GTA GGA CTC CTG AAT CCA CTC CTG TCT TTT CCC GTC ACG  
 Cys Cys Leu Leu Phe Val Gly Leu Leu Asn Pro Leu Leu Ser Phe Pro Val Thr  
 .....→ .....

## peptide signal

117            126            135            144            153            162  
 GAC ACT GGT GAA ATG TCT CTT CAG CTT CCA GTG CTT GAG GAA AAT GCT CTT CGG  
 Asp Thr Gly Glu Met Ser Ieu Gln Leu Pro Val Leu Glu Asn Ala Leu Arg  
 .....→ .....

171            180            189            198            207            216  
 GCT CTG GAG GAG CTG GAG AGG ACT GCC CTC CTG CAG ACG CTG CGC CAG ACC GTG  
 Ala Leu Glu Glu Leu Glu Arg Thr Ala Leu Leu Gln Thr Leu Arg Gln Thr Val  
 .....→ .....

## pro-segment

225            234            243            252            261            270  
 GGC ACA GAA GCA GAG GGA AGC CTT GGC CAG GCA GAT CCC AGT GCC GAG ACT CCC  
 Gly Thr Glu Ala Glu Gly Ser Leu Gly Gln Ala Asp Pro Ser Ala Glu Thr Pro  
 .....→ .....

279            288            297            306            315            324  
 ACT CCA AGG GGA AGC TTG AGG AAG GCT CTC ACT GGG CAA GAT TCT AAC ACT GTA  
 Thr Pro Arg Gly Ser Leu Arg Lys Ala Leu Thr Gly Gln Asp Ser Asn Thr Val  
 .....→ .....

333            342            351            360            369            378  
 CTG AGC CGT CTT TTG GCG AGA ACC AGG AAA CAA CGT AAG CAA CAC GGG ACT GCC  
 Leu Ser Arg Leu Leu Ala Arg Thr Arg Lys Gln Arg Lys Gln His Gly Thr Ala  
 .....→ .....

387            396            405            414            423            432  
 CCA GAA TGC TTC TGG AAG TAC TGC ATT TCA AGA GAG ACG TCT CCT CAG AAC CAT  
 Pro Glu Cys Phe Trp Lys Tyr Cys Ile \*\*\*  
 → .....

## UrotensineII

441            450            459            468            477            486  
 CAC TTC AGG AAA CTA AAG AGC ACA TGC TTG AAG AAA AAT CGT GCC AAC AAC GCC

495            504            513            522  
 CCG TTC TCC ACT ATG AGA AAT AAA CCC TCT ATG TTT CTC AAC T 3'

FIGURE 3

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9            18            27            36            45            54  
 5' CCA GAG CAG ACG CCC AGA CGG ACT TCT CGC CGC ATC ATG GAC AGG GTG CCC TTC  
 Met Asp Arg Val Pro Phe



63            72            81            90            99            108  
 TGC TGC CTG CTC TTC ATA GGA CTT CTG AAT CCA CTG CTG TCC CTT CCC GTC ACG  
 Cys Cys Leu Leu Phe Ile Gly Leu Leu Asn Pro Leu Leu Ser Leu Pro Val Thr


**peptide signal**

117            126            135            144            153            162  
 GAC ACT GGT GAG AGG ACT CTT CAG CTT CCA GTG CTT GAG GAA GAC GCT CTT CGG  
 Asp Thr Gly Glu Arg Thr Leu Gln Leu Pro Val Leu Glu Glu Asp Ala Leu Arg



171            180            189            198            207            216  
 GCT CTG GAG GAG CTG GAG AGG ATG GCC CTC CTG CAG ACC CTG CGT CAG ACC ATG  
 Ala Leu Glu Glu Leu Glu Arg Met Ala Leu Gln Thr Leu Arg Gln Thr Met


**pro-segment**

225            234            243            252            261            270  
 GGC ACG GAA GCA GGG GAG AGC CCT GGA GAA GCA GGT CCC AGC ACT GAG ACT CCC  
 Gly Thr Glu Ala Gly Glu Ser Pro Gly Glu Ala Gly Pro Ser Thr Glu Thr Pro



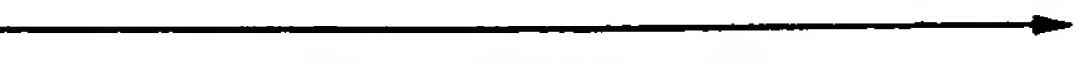
279            288            297            306            315            324  
 ACT CCA CGG GGA AGC ATG AGG AAG GCT TTC GCT GGG CAA AAT TCT AAC ACT GTA  
 Thr Pro Arg Gly Ser Met Arg Lys Ala Phe Ala Gly Gln Asn Ser Asn Thr Val



333            342            351            360            369            378  
 CTG AGT CGT CTC TTG GCA AGA ACC AGG AAA CAA CAT AAG CAA CAC GGG GCT GCC  
 Leu Ser Arg Leu Ala Arg Thr Arg Lys Gln His Lys Gln His Gly Ala Ala



387            396            405            414            423            432  
 CCA GAG TGC TTC TGG AAA TAC TGC ATT TGA GGA GAC ACA AGC GCC CGT TGG TCT  
 Pro Glu Cys Phe Trp Lys Tyr Cys Ile \*\*\*


**Urotensine II**

441            450            459            468            477            486  
 CTC AGA ACC ATT ACA TTC AGG AAA CGG GCA GAG CAG ATG CTT GAA GCA AAA TCA

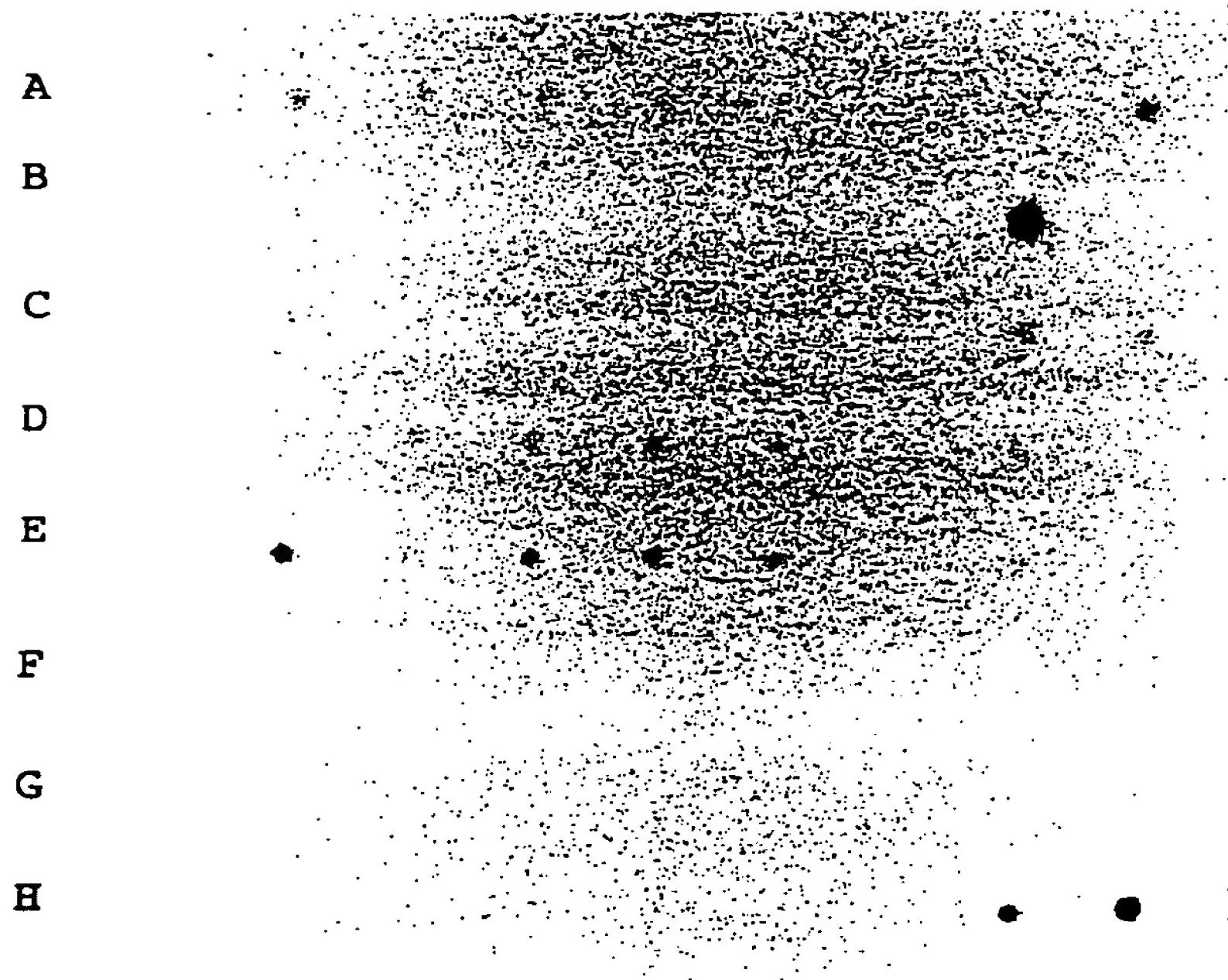
495            504            513            522            531  
 CGC TAA CGA CGC CTT GTT CTT CAT TAT GAG AAA TAA ATC CTC TAT GTT TCT CA 3'

**FIGURE 4**

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**A**

1 2 3 4 5 6 7 8

A  
B  
C  
D  
E  
F  
G  
H

	1	2	3	4	5	6	7	8
A	cerveau entier	amygdales	noyau caudé	cervelet	cortex cérébral	lobe frontal	hippocampe	<i>medulla oblongata</i>
B	lobe occipital	putamen	<i>locus niger</i>	lobe temporal	thalamus	noyau sous-thalamique	moelle épinière	-
C	cœur	aorte	muscle squelettique	colon	vessie	utérus	prostate	estomac
D	testicules	ovaires	pancréas	hypophyse	glande surrénale	thyroïde	glande salivaire	glande mammaire
E	rein	foie	intestin grêle	rate	thymus	leucocyte périphérique	ganglion lymphatique	moelle osseuse
F	appendice	poumon	trachée	placenta	-	-	-	-
G	cerveau foetal	cœur foetal	rein foetal	foie foetal	rate foetale	thymus foetal	poumon foetal	-
H	ARN total de levure 100 ng	ARNt de levure 100 ng	ARNr d' <i>E. coli</i> 100 ng	ADN d' <i>E. coli</i> 100 ng	poly r(A) 100 ng	ADN C <sub>ot</sub> I humain	ADN humain 100 ng	ADN humain 500 ng

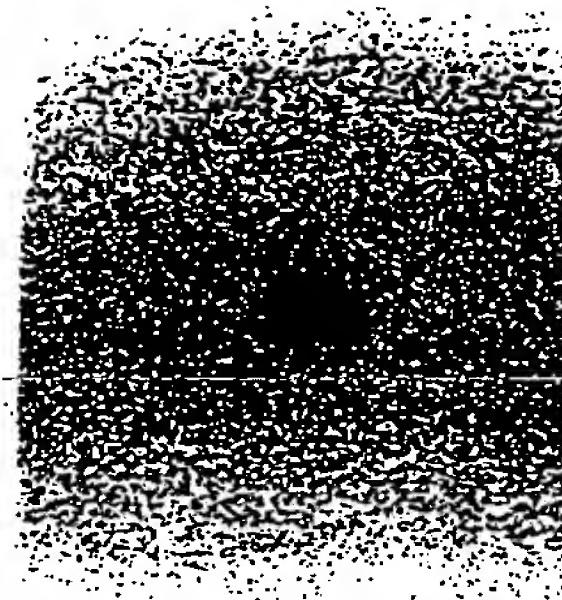
FIGURE 5.1

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B

moelle  
épinière

725 pb →



C



(1)



(2)

FIGURE 5.2

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FIGURE 6

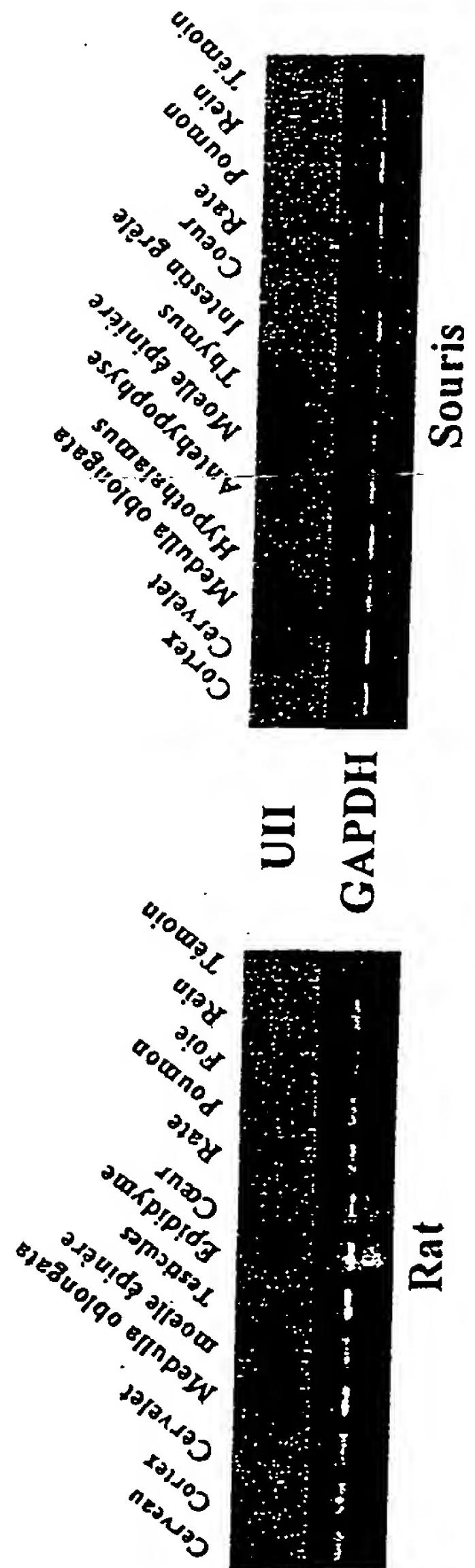


FIGURE 7